

22 107.4 5.0 259498 61 AC020876
23 104.8 4.9 731 77 CNSOIFEV
24 100.4 4.6 11886 1 AE004638
25 94.8 4.4 110000 71 AC078913_1
26 87.6 4.1 41807 29 SC6D11
27 84.6 3.9 16164 1 AE004094
28 72.6 3.4 1713 81 A07753
29 71.8 3.3 15657 1 AE001730
30 69.8 3.2 96086 29 STYSTMD1
31 67.4 3.1 231916 73 AL158037
32 66.4 3.1 146174 2 D90910
33 64.2 3.0 13725 1 AE000832
34 62.4 2.9 1788 1 AF091510
35 62.4 2.9 7045 2 ECPROM
36 62.4 2.9 7203 2 ECOLILVGMED
37 62.4 2.9 8088 2 ECOLILVGMED
38 62.4 2.9 14325 1 AE000453
39 62.4 2.9 91414 2 ECOMW85
40 60.8 2.8 2343 2 ECOLVX
41 60.8 2.8 2841 21 E10718
42 60.8 2.8 2841 81 AR092608
43 60.8 2.8 2841 81 E13058
44 60.8 2.8 4900 2 ECOMRNILV
45 60.8 2.8 9456 2 ECOLVGE

ALIGNMENTS

1
RESULT SCIA9 29400 bp DNA BCT 11-DEC-1998
LOCUS Streptomyces coelicolor cosmid 1A9.
SCL1A9 AL034446
DEFINITION ADA-like regulatory protein; arac family; gntR; helix-turn-helix;
VERSION His rich; integral membrane; luxR; luxR family;
ACCESSION methylated-DNA-protein-cysteine methyl transferase; nucleotide
KEYWORDS binding; ogt; oxidoreductase; poxB; pyruvate oxidase; response
regulator; sensor kinase; sorbitol oxidase; thiamine
pyrophosphate; TPP; transferase; transmembrane protein; two
component system.
SOURCE Streptomyces coelicolor A3(2).
ORGANISM Streptomyces coelicolor A3(2).

REFERENCE Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
AUTHORS Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
JOURNAL 1 (bases 1 to 29400)
REFERENCE Saunders,D.C. and Harris,D.
AUTHORS Unpublished
TITLE 2 (bases 1 to 29400)
JOURNAL Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1998) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
REFERENCE 3 (bases 1 to 29400)
AUTHORS Redenbach,M., Kieser,H.M., Denapante,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
TITLE A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
JOURNAL Mol. Microbiol. 21 (1), 77-96 (1996)
MEDLINE 97000351
COMMENT Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC.
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
(URL: <http://www.sanger.ac.uk/Projects/S-coelicolor/>) CDS are
numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at <http://www.nih.go.jp/jun/cgi-bin/frameplot.pl>. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or att) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 1A9 lies between 9B2 and 6C5 in the Ase-I-B genomic restriction fragment.

FEATURES

Location/Qualifiers
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/strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid 1A9"
complement(1..651)
/gene="SC1A9.01c"
complement(<1..651)
/gene="SC1A9.01c"
/note="SC1A9.01c, incomplete CDS, possible transferase, partial CDS, len: 219 aa, similar to TR:O53185 (EMBL:AL021246) a proposed transferase from Mycobacterium tuberculosis (302 aa), fasta scores: Opt: 764, z-score: 1097.3, E(): 0, (62.1% identity in 203 aa overlap (302 aa). Also weakly similar to several methyltransferases eg. MTHF, ECOLI
(EMBL:X16584)5-methyltetrahydrofolate-homocysteine methyltransferase (1226 aa), fasta scores: Opt:160, z-score: 234.8, E(): 8.4e-06, (30.0% identity in 220 aa overlap)."
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/db_xref="GI:4007686"
/translation="MTSDFADALASGLVLDGGLSNQLEAAGHLDGALWSARLLAEAD PEATRAHLAYFEAGAEVAITSSYQATFEFGARRGIGRERAAELLALSASAREARR ARTAPRALWVAASGAPYCAMIADGSEYRGYGLGRGALERHPRLEVLAAAPDV LALETVPDTEAAALLRAVRLDVPANLSYTVAGDTRAGQPLDEAFALAAADVETI"
731..1654
/gene="SC1A9.02"
/note="SC1A9.02"
731..1654
/gene="SC1A9.02"
307aa; Contains several possible membrane spanning domains."
/codon_start=1
/transl_table=11
/product="putative transmembrane protein"
/protein_id="CAA22372.1"
/db_xref="GI:4007687"
/translation="MTISGRRTKSRVCSRHSHGDEGVPVRFVWQFLAVLVAYAIAG GIAVQAKNDMLTVLTVSVLVYVAVVWVVRTERRELDALDLSVASAREAGTIL IGFLEFAGVITNLFASGYDGLGVOAGIAGLWGPMAAAATEEVFVFGVLFRIIEE HIGTYLALGLTGLVFCGLMHLNEDATLWALAIADGAFMLAAAYATRNMLTGVH FGWNPAGGVSTVSGNGDSGLDMSGPKLLTGGDFGPGEGSVYISVFGVGLTTLV FWLAAHRRGNIVAFGSRRAAGANSATLPR"
1651..2817
/gene="SC1A9.03"

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1651. .2817
/ gene="SCIA9.03"
/ note="SCIA9.03, probable two component sensor kinase,
len: 388aa; similar to a family of sensor kinases egs.
TR:Q53893 (EMBL:U51332) AbsA1 from Streptomyces coelicolor
(571 aa), fasta scores: opt: 389, z-score: 278.9, E():
2.9e-08, (33.1% identity in 405 aa overlap) and UHPB_ECOLI
(EMBL:M17102) sensor kinase from Escherichia coli (500
aa), fasta scores: opt: 221, z-score: 248.0, E(): 1.5e-06,
(25.9% identity in 398 aa overlap). Contains several
possible membrane spanning domains."
/codon_start=1
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/product="putative sensor kinase"
/protein_id="CAA22373.1"
/db_xref="GI:4007688"
/translation="NIDRRVLELRRLDVTVRDPLGVLLLVASLLPSLRQGTGIG
GLTPRPADALGAVAVQSIPIAVRRMTLLCLTSLVSGFALDQLRAYHLFAGAAALPI
VLINAGSHEQRYRATQVATIGYVAMAVGLNARGDDELVEYTFYLVLAAMGPI
WMSARAAEARRSVAEDARNARTRIARELDHVVTHVTVAMVQSAARYLTAAP
RDESLAAVSDTGRRAITDLRHLLDHPDHTAPRTPPVGRVLTLLVEOTRACGPV
EFTEGTAAATGSSDLVAVRVQEAALNALKYDHGRTSLVRHGEREITVEVGTG
SGSAAASGCGSGLAGLRERVDVLGGEFSDRDPADGFFVVRARIPGSGGSTA"
2814. .3473
/ gene="SCIA9.04"
2814. .3473
/ gene="SCIA9.04"
/ note="SCIA9.04, probable luxR family response regulator,
len: 219 aa; similar to a family of regulators egs.
TR:O09816 (EMBL:AL023496) probable two-component regulator
from Streptomyces coelicolor (224 aa) fasta scores:
opt: 714, z-score: 1103.5, E(): 0, (54.8% identity in 219 aa
overlap) and NARL_ECOLI (EMBL:X13360) nitrate/nitrite
response regulator from Escherichia coli (216 aa) fasta
scores: opt: 455, z-score: 656.5, E(): 2.7e-29, (37.6%
identity in 213 aa overlap). Contains pfam match to entry
PF00072 response_reg, Response regulator receiver domain,
score 111.10, E-value 2.1e-29, Pfam match to entry PF00196
GerE, Bacterial regulatory proteins, luxR family, score
79.50, E-value 7e-20, PS00622 Bacterial regulatory
proteins, luxR family signature and an helix-turn-helix
motif from: 1 to: 219, Score 983 (+2.53 SD)."
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/protein_id="CAA22374.1"
/db_xref="GI:4007689"
/translation="MSAPIRVVICDDQALIFRTGLATIVDAQDLEVVGECDGQGTGVD
LARELPDVMIDIMPVLVDGLEATRLLAGACVAHPVKVVLVVTFFNLDEYVVEALRAG
ASGFLKDPAPDRLRLHGRITVAMGAALLDPDVTBRLVGRYARIRPAEGTARDILTP
RTEVLRLIADGLSNEIAALVISPEVTKTFVSRILFKLDLRQVAVFYRHLV
T"
2826. .3173
/ gene="SCIA9.04"
/ note="pfam match to entry PF00072 response_reg, Response
regulator receiver domain, score 111.10, E-value 2.1e-29"
3276. .3470
/ gene="SCIA9.04"
/ note="pfam match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 79.50, E-value
7e-20"
3327. .3410
/ gene="SCIA9.04"
/ note="PS00622 Bacterial regulatory proteins, luxR family
signature."
complement(3492..4094)
/ gene="SCIA9.05c"
complement(3492..4094)
/ gene="SCIA9.05c"
/ note="SCIA9.05c, possible transmembrane protein, len: 200
aa; contains possible membrane spanning hydrophobic
regions"
/codon_start=1

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/product="putative transmembrane protein"
/protein_id="CAA22375.1"
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GYMALAGVVRVLNLTGTSAMLSALLGAVPAAVWTVVWVRRRVDRADAVGAEPDVP
AMEROILKGGGPAPRPPERRRMAAFVDSROERLRNRWMAFPLAVIFFGTSALWYLS
GSVGAGSLMLGILGVVFLGLWLAWNLRIDRLRSHMRKRLRG"
4140. .4631
/ gene="SCIA9.06"
4140. .4631
/ gene="SCIA9.06"
Query Match 24.6%; Score 532.4; DB 29; Length 29400;
Best Local Similarity 58.0%; Pred. No. 9.8e-131;
Matches 1020; Conservative 0; Mismatches 726; Indels 12; Gaps 4;
QY 332 acacagctacgcagagaacaatttaattgacacatttggaagctcaaggtgtgaagcaattta 391
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18101 ACAGAACGTCGCGGAACAGTTCGTCACATCTCACCCGCGCGGGTTCGAGCGCCTCTA 18160
QY 392 tgggttggtgggtgacagaccttaattccgacatcggtggtgctgt---ccgccaalacagatat 448
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18161 CGAGTCTGCGGACAGCCTCAACCCCTGCTGGAGCGCGTTCGCGCGCATTCGCGCAT 18220
QY 449 tgaagtggtgacgcttcgaaatgaggaagcgcggttgcaagcgggtgcggaaatcgtt 508
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18221 CGAATGGGTGACAGTACGACAGCAGGAGACCGCGCTTCGCGCGCGGAGCGCA 18280
QY 509 gatactgggagctggcgagtgatgctgctctcttctgctgctggaacacacacactgatt 568
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18281 GATCACCGGGAAGCTCACCGCTGCGCGCTCTCTCGCGCGCGGAACTCCACCTCAT 18340
QY 569 tcagggtctttatgattcgcatcgaaatggtgcgaaggtggtggcctcgctagccatat 628
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18341 CAACGGCTCTAGCAGCGCCACCGCTCCATGGCCCCCGTCTCGCCCTGCCAGAT 18400
QY 629 tcgagtgccagagattggttcgacttcttcaggaagaaacgacatcccgagattttgttaa 688
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18401 CCGCTCCAGCAGAGATCGGCTCGGCTTCTTCCAGAGAGACACCCCGACAGCTGTTCG 18460
QY 689 ggaatgctgtggttactcgagatggtgaatggtgagcagaggtgaaacgacttttga 748
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18461 CGAGTGCAGTCACTACAGGAGCTGATCTCCAGCCCGAGAGATGCCCGGCTGCTCCA 18520
QY 749 tcacgcatttcagtcacacacatgcggtgtaaaagtggtggtggtgattctctgtgta 808
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Db 18521 GACCGCATCCAAACACGCGCTGCGCCAGGCGCGGTACGGTCTGCTCGCTGCCCGCCA 18580
QY 809 tatcgtaagggaagacgaggtgacggttacttattccaatccactatttctcttggcac 868
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18581 CATCGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18640
QY 869 tctgtggtgttcccgagatcctactgagctcagcgctggtgagcggtataaacaagc 928
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18641 CACCGTCCCG---CCCGCGCAGCAGAGATGACCGCGCTGCTCGCGATGATCGACCGC 18697
QY 929 taagtctgtaactttgttctgctggtggtggtggtggtggtggtggtggtggtggtg 988
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18698 CGACAAGGTCACTCTTCTGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18757
QY 989 gttgaggaagattaaatcaccatcggtggtggtggtggtggtggtggtggtggtggtg 1048
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18758 GTTCGCGGGAAGCTCAAGCGACCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 18817
QY 1049 gcatgagaatccggttggtggtggtggtggtggtggtggtggtggtggtggtggtg 1108
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18818 GTACGACACCGCTACGACCTCGGCGATGACCGACCTGCTCGCGCTACGCGCGCGCT 18877
QY 1109 tgcgtccaatgagggcggtggtggtggtggtggtggtggtggtggtggtggtggtg 1168
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18878 GGCCACCCAGCTCGGACCTGCTGCTCTGATCGGACCGACTTCCTCCCTACACGCCCTT 18937

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Qy 1169 ccttctaaagac---aacgttcccaggtggatatacaacggtgagcacattggtgagc 1225
Db 18938 CCTCCGGACACGTGAAGATCCCAAGATCGCTGCGGCCAGACACCTGGAGCGGC 18997
Qy 1226 tacacaggtgaagtatccgtgaccgtggtggtgctgcaacaatgaaatattttgcc 1285
Db 18998 CTCACAGCTGGACTCCGGTGTGGGCGACGCGCGGAGACGCTGCGCTGCCTGATCCC 19057
Qy 1286 tcattgaagaaacacagatgcttcttcccttgatcggtatgctcaagacacagcg 1345
Db 19058 CCGGCTCAAGAGAGAAACACCGCTCTCTGACCGGATGCTGAAGACGACGCGGA 19117
Qy 1346 taagttagctcgggtgtagagacgacacacataacgctgagagcagatgctgctattca 1405
Db 19118 CGCCCTGAAGCGTCTGCTCAAGGGCTACACCGCAAGGTGACACAGCAGCTGCCGATCCA 19177
Qy 1406 cccgaatacagctccctctattttgaacagcgtggtgataaggtgctggtttactgt 1465
Db 19178 CCGCGAGTACGTGGCGGCCCTGCTGGAGAGATGCGCGACGACGCGGTTTCACCGT 19237
Qy 1466 gataccggcatgtgcaatgtgtgcatgctgaggtgacatcgagaaatccggaggaacg 1525
Db 19238 CGACACCGGATGTCACAGCTGTGGCGGCTGCTTACATCTCG---CCCAACGGCGCG 19294
Qy 1526 cgacttgggtggttattccgcacgacgacgacgacgacgacgacgacgacgacgacg 1585
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Qy 1586 tgcgcaaggtgtgacgaaacgacgacgacgacgacgacgacgacgacgacgacgacg 1645
Db 19355 CGCCCAAGTACCGACCGCGCGGACAGCTGCTGCGATGTCGCGGACGCGGCTTCA 19414
Qy 1646 catgctgctgggtgagcttctgacggttaagctgacacacacacacacacacacacac 1705
Db 19415 CATGCTGATGGCGGACTTCTTCAACCTCTCCAGCAGCAGCTGCCGCTGCGGATCGT 19474
Qy 1706 gtttaacacagttcttgggacggtgaggtgaggtgaggtgaggtgaggtgaggtgag 1765
Db 19475 CTTCAACAACTCTCGCTCGGCAATGCTGAGTGGAGATGCTGCTGCGGCGCTGCCCTC 19534
Qy 1766 attgtgactgacacaggaaggtgatttcgagagattggtggtggtggtggtggtggt 1825
Db 19535 GCACGGGTGGCCCAACAGAACCCGAGCTTCCGCGCGCTGCGCGAGGCTGCGCGGCTT 19594
Qy 1826 atcggtacgacacacgac 1885
Db 19595 CGGCTCGGGTGGAGAAGCCCAAGGACCTGGCGGGCGCTGAAGGCGGCTTCAAGCA 19654
Qy 1886 tcctggacctgactgacgacacacacacacacacacacacacacacacacacacac 1945
Db 19655 CAAGGTCCGCGCTCTGCGACGCTGTCACCGACCCCAAGCGCTGTCATCCCGCGGAA 19714
Qy 1946 catcacgtggaaacagctcaggtgattcagaaagcgccacacacacacacacacacac 2005
Db 19715 GATCAGCGCCGACATGTCACCGCTTTCGCGCTTTCGCGCTGCGAGATGCTGCTGGACG 19774
Qy 2006 aggaatgagcgatgacgac 2065
Db 19775 CGGGTTCGAGCGATGCTCCAGATGGCGCGCTGCAACCTGCGCAACGTCGCGCGCGCGT 19834
Qy 2066 atgattgatacactgct 2083
Db 19835 ACCGTACGACAGCGCGT 19852

RESULT 2
ECPOXB 1974 bp DNA BCT 12-SEP-1993
LOCUS E. coli poxB gene for pyruvate oxidase.
DEFINITION X04105 M13947 M13948
ACCESSION X04105.1 GI:42472
VERSION
FEATURES
flavoprotein; inverted repeat; poxB gene; pyruvate oxidase.

SOURCE Escherichia coli.
ORGANISM Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
REFERENCE 1 (bases 1 to 1974)
AUTHORS Grabau,C. and Cronan,J.E. Jr.
TITLE Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate oxidase, a lipid-activated flavoprotein
JOURNAL Nucleic Acids Res. 14 (13), 5449-5460 (1986)
MEDLINE 86286555
COMMENT Data kindly reviewed (31-MAY-1987) by C. Grabau.
FEATURES
source Location/Qualifiers
1. 1974
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/strain="K12"
/db_xref="taxon:562"
56..64
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73..81
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164..168
/note="put. ribosome binding site"
179..1897
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MSTRHEEVAFAAFAEAQSLGELAVAGSCGPNLHNLGLFDCRHRNPVPLATAAHI
PSSIGSGYFOETHPELRECSHYCELVSPPEOIPVOLAIAHRKALVNRGVVVLV
GDVALKPAPEGATMHVHAPQVPTPEEELRKLQALLRYSNLALMCGSCGAHKE
LYEPAGTKAPIVHALRGKEHVEYDNPVDMGLIGFSGFHTMNAADTLVLGTQF
PVAFYPTDAKIIOIDINPASIGAHKVDMAVGLDIKSTLRALLPLVEEKADRRFLDK
ALEYDRARKGLDLAKPSEKAIHPOYLAQOISHPAADDALFTCDVGTPTVMAAYLK
MNGKRRLLGNSHNIGSMANNPQALGAQATPEROVVAMCGSGFSLMGDFLSVYOMK
LPVXIVFVNSVLGVAMEMKAGLYLTDGTEHDTNFARIAEGGIGTIRVEKASEVD
EALQRAFSDIGPVLVDVVVAVBEALPQIILEQAKGFSLYMLRAILISGRGDEVIELA
KTNMLR"
BASE COUNT 474 a 521 c 535 g 444 t
ORIGIN
Query Match 14.1%; Score 305.2; DB 2; Length 1974;
Best Local Similarity 50.7%; Pred. No. 3e-70;
Matches 873; Conservative 0; Mismatches 828; Indels 21; Gaps 5;
Qy 327 atggcacacagctacgcagaaacaaattaattgacacatttggaaagctcaaggtggaagcga 386
Db 179 ATGAACAAACCGTTCGAGCTTATCGCCAAACACACTCGCAATCGCGAGGGGTGAACGC 238
Qy 387 atttatggttgggtgagcagccttaa---tccgacgtggatgctgctccgccaatca 443
Db 239 ATCTGGGAGTACACAGCGACTCTCTGAACGGCTTTAGTCACACTCTTAATCGCATGGGC 298
Qy 444 gataatgagtggtgacgcttcgaaatgagaaagcgcgctttgagcgcggtgagaa 503
Db 299 ACCATCGAGTGGATGTCACCGCCGACGAGAGAGTGGCGGCTTTGCGGCTGGCGCTGAA 358
Qy 504 tcggttgactcactgggagctgagtgatgctgctcttctggtctctctgagaaacacacac 563
Db 359 GCACAACCTAGCGGAGAACTGGCGGTCTGCGCGGATGCTGCGCGCCCGCGGAACCTGCAC 418
Qy 564 ctgattcaggtcttattgattcgcacgaaatggtgcgaaggtgtggtccatcgctagc 623
Db 419 TTAATCAACGGCTGTTCGATGGCCACCGCAATCAGCTTCCTGGTACTGGCGCTTGGCGCT 478
Qy 624 catattccgagtgccagatggttcgcagcgttcttccaggaaacacgcatcccgagattttg 683
Db 479 CATATTCCCTCCAGCGAAATGGCAGCGGCTATTTCAGGAGAAACCCACCCACAGAGCTA 538
Qy 684 tttaaggaatgctctggttactgagagatggtgaatggtgagcaggggtgaacgcatt 743